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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO	
10/712,629	11/13/2003	Kotikanyadanam Sreekrishna	9423	5723	
27752	7590 06/13/2006	EXAMINER			
	TER & GAMBLE CO	DUNSTON, JE	DUNSTON, JENNIFER ANN		
	UAL PROPERTY DIVI LL TECHNICAL CENT	ART UNIT	PAPER NUMBER		
6110 CENTE	R HILL AVENUE	1636			
CINCINNAT	TI, OH 45224	DATE MAILED: 06/13/2006			

Please find below and/or attached an Office communication concerning this application or proceeding.



UNITED STATES DEPARTMENT OF COMMERCE U.S. Patent and Trademark Office

Address: COMMISSIONER FOR PATENTS

P.O. Box 1450

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10 712,629

APPLICATION NO./ FILING DATE FIRST NAMED INVENTOR / ATTORNEY DOCKET NO. PATENT IN REEXAMINATION

EXAMINER

ART UNIT

PAPER

20060609

DATE MAILED:

Please find below and/or attached an Office communication concerning this application or proceeding.

Commissioner for Patents

This application contains sequence disclosures that are encompassed by the definitions for nucleotide and/or amino acid sequences set forth in 37 CFR 1.821(a)(1) and (a)(2). A computer readable form (CRF) of the sequence listing was submitted. However, the CRF could not be processed by the Scientific and Technical Information Center (STIC) for the reason(s) set forth on the attached CRF Diskette Problem Report.

Applicant is given ONE MONTH, or THIRTY DAYS, whichever is longer, from the mailing date of this letter within which to comply with the sequence rules, 37 CFR 1.821 - 1.825. Failure to comply with these requirements will result in ABANDONMENT of the application under 37 CFR 1.821(g). Extensions of time may be obtained by filing a petition accompanied by the extension fee under the provisions of 37 CFR 1.136(a). In no case may an applicant extend the period for reply beyond the SIX MONTH statutory period. Direct the reply to the undersigned. Applicant is requested to return a copy of the attached CRF Diskette Problem Report with the reply.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Jennifer Dunston whose telephone number is 571-272-2916. The examiner can normally be reached on M-F, 9 am to 5 pm.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Remy Yucel can be reached at 571-272-0781. The fax phone number for the organization where this application or proceeding is assigned is 571-273-8300.

Any inquiry of a general nature or relating to the status of this application or proceeding should be directed to (571) 272-0547.

Patent applicants with problems or questions regarding electronic images that can be viewed in the Patent Application Information Retrieval system (PAIR, http://pair-direct.uspto.gov) can now contact the USPTO's Patent Electronic Business Center (Patent EBC) for assistance. Representatives are available to answer your questions daily from 6 am to midnight (EST). The toll free number is (866) 217-9197.

For all other customer support, please call the USPTO Call Center (UCC) at 800-786-9199.

CELINE QIAN, PH.D. PRIMARY EXAMINER

Jennifer Dunston Examiner Art Unit 1636

Application No. Applicant(s) 10/712,629 Kotikanvadanam et al. **Notice to Comply** Examiner Art Unit Jennifer Dunston 1636 NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE **DISCLOSURES** Applicant must file the items indicated below within the time period set the Office action to which the Notice is attached to avoid abandonment under 35 U.S.C. § 133 (extensions of time may be obtained under the provisions of 37 CFR 1.136(a)). The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s): 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to the final rulemaking notice published at 55 FR 18230 (May 1, 1990), and 1114 OG 29 (May 15, 1990). If the effective filing date is on or after July 1, 1998, see the final rulemaking notice published at 63 FR 29620 (June 1, 1998) and 1211 OG 82 (June 23, 1998). ☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c). 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e). 🛛 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing." 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d). 6. The paper copy of the "Sequence Listing" is not the same as the computer readable from of the "Sequence Listing" as required by 37 C.F.R. 1.821(e). ☐ 7. Other: Applicant Must Provide: An initial or substitute computer readable form (CRF) copy of the "Sequence Listing". An initial or substitute paper copy of the "Sequence Listing", as well as an amendment specifically directing its entry into the application. A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216 or (703) 308-2923

For CRF Submission Help, call (703) 308-4212 or 308-2923

Patentin Software Program Support

Technical Assistance......703-287-0200
To Purchase Patentin Software......703-306-2600

PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR REPLY

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number:	10/7/2.6290
Source:	1Fw16
Date Processed by STIC:	5/2/06

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE <u>CHECKER</u> <u>VERSION 4.4.0 PROGRAM</u>, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

- 1. EFS-Bio (http://www.uspto.gov/ebc/efs/downloads/documents.htm, EFS Submission User Manual ePAVE)
- 2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
- 3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):
 U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street,
 Alexandria, VA 22314

Revised 01/10/06

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION SERIAL NUMBER: 10/7/2, 629C
ATTN: NEW RULES CASES:	PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE
lWrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
2Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.
3Misaligned Amino Numbering	The numbering under each 5 th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
4Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
5Variable Length	Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
6PatentIn 2.0 "bug"	A "bug" in Patentln version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) Normally, Patentln would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
7Skipped Sequences (OLD RULES)	Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
8Skipped Sequences (NEW RULES)	Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000
9Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
10 Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence. (see item 11 below)
11Use of <220>	Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown Please explain source of genetic material in <220> to <223> section or use "chemically synthesized" as explanation. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of Sequence Rules
Patentin 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
13 Misuse of n/Xaa	"n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid



IFW16

RAW SEQUENCE LISTING DATE: 05/02/2006
PATENT APPLICATION: US/10/712,629C TIME: 14:30:25

Input Set : A:\PTO.TS.txt

Output Set: N:\CRF4\05022006\J712629C.raw

```
3 <110> APPLICANT: The Procter & Gamble Company
     5 <120> TITLE OF INVENTION: Composition Comprising a Mouse HRt Protein Human
             Interacting Partner Protein Complex
                                                            on 1,3-5
     8 <130> FILE REFERENCE: 9423
    10 <140> CURRENT APPLICATION NUMBER: US 10/712,629C
    11 <141> CURRENT FILING DATE: 2003-11-13
    13 <160> NUMBER OF SEQ ID NOS: 20
    15 <170> SOFTWARE: PatentIn version 3.3
                                                             Does Not Comply
                                                             Corrected Diskette Needed
                                693 (p.3)
ERRORED SEQUENCES
    523 <210> SEQ ID NO: _17
    524 <211> LENGTH: (2079)
    525 <212> TYPE: ONA)! This is a PRT sequence
    526 <213> ORGANISM: Nucleotide sequence of HRt corresponding to the amino acid residue
    527/1182 of the C-terminal portion of HR protein
    529 <400> SEQUENCE: 17
    531 Val Thr Gln Cys Gln Ser Cys Val Gln Ala Ala Gly Glu Val Gly Val
    535 Leu Thr Gly His Ser Gln Lys Ser Arg Arg Ser Pro Leu Glu Glu Lys
                    20
                                        25
    539 Gln Leu Glu Glu Glu Asp Ser Ser Ala Thr Ser Glu Glu Gly Gly
                                                        45
                                    40
    543 Gly Pro Gly Pro Glu Ala Ser Leu Asn Lys Gly Leu Ala Lys His Leu
                                55
    547 Leu Ser Gly Leu Gly Asp Arg Leu Cys Arg Leu Leu Arg Lys Glu Arg
                            70
                                                75
                                                                    80
    551 Glu Ala Leu Ala Trp Ala Gln Arg Glu Gly Gln Gly Pro Ala Met Thr
    555 Glu Asp Ser Pro Gly Ile Pro His Cys Cys Ser Arg Cys His His Gly
                                        105
    556
    559 Leu Phe Asn Thr His Trp Arg Cys Ser His Cys Ser His Arg Leu Cys
                                    120
    563 Val Ala Cys Gly Arg Ile Ala Gly Ala Gly Lys Asn Arg Glu Lys Thr
                                135
    567 Gly Ser Gln Glu Gln His Thr Asp Asp Cys Ala Gln Glu Ala Gly His
                                                155
                            150
    571 Ala Ala Cys Ser Leu Ile Leu Thr Gln Phe Val Ser Ser Gln Ala Leu
                                            170
    575 Ala Glu Leu Ser Thr Val Met His Gln Ala Trp Ala Lys Phe Asp Ile
                                        185
```

579 Arg Gly His Cys Phe Cys Gln Val Asp Ala Arg Val Trp Ala Pro Gly

RAW SEQUENCE LISTING DATE: 05/02/2006
PATENT APPLICATION: US/10/712,629C TIME: 14:30:25

Input Set : A:\PTO.TS.txt

Output Set: N:\CRF4\05022006\J712629C.raw

580			195				_	200		_			205			
583	Asp	Gly	Gly	Gln	Gln	Lys		Pro	Thr	Glu	Lys	Thr	Pro	Pro	Thr	Pro
584		210					215					220				
587	Gln	Pro	Ser	Cys	Asn	Gly	Asp	Ser	Asn	Arg	Thr	Lys	Asp	Ile	Lys	Glu
588	225					230					235					240
591	Glu	Thr	Pro	Asp	Ser	Thr	Glu	Ser	Pro	Ala	Glu	Asp	Gly	Ala	Gly	Arg
592					245		•			250					255	
595	Ser	Pro	Leu	Pro	Cys	Pro	Ser	Leu	Суз	Glu	Leu	Leu	Ala	Ser	Thr	Ala
596				260					265					270		
599	Val	Lys	Leu	Cys	Leu	Gly	His	Asp	Arg	Ile	His	Met	Ala	Phe	Ala	Pro
600			275					280					285			
603	Val	Thr	Pro	Ala	Leu	Pro	Ser	Asp	Asp	Arg	Ile	Thr	Asn	Ile	Leu	Asp
604		290					295			_		300				
607	Ser	Ile	Ile	Ala	Gln	Val	Val	Glu	Arg	Lys	Ile	Gln	Glu	Lys	Ala	Leu
608	305					310			_	_	315			_		320
611	Gly	Pro	Gly	Leu	Arg	Ala	Gly	Ser	Gly	Leu	Arg	Lys	Gly	Leu	Şer	Leu
612	•		•		325		•		-	330	-	-	-		335	
615	Pro	Leu	Ser	Pro	Val	Arg	Thr	Arg	Leu	Ser	Pro	Pro	Gly	Ala	Leu	Leu
616				340		Ū			345				-	350		
619	Trp	Leu	Gln	Glu	Pro	Arq	Pro	Lys	His	Gly	Phe	His	Leu	Phe	Gln	Glu
620	-		355			٠ -		360		-		•	365			
623	His	Trp	Arg	Gln	Gly	Gln	Pro	Val	Leu	Val	Ser	Gly	Ile	Gln	Lys	Thr
624		370	_		•		375					380			•	
	Leu	Arq	Leu	Ser	Leu	Trp	Gly	Met	Glu	Ala	Leu	Gly	Thr	Leu	Gly	Gly
	385	•				390	•				395	•			•	400
		Val	Gln	Ser	Leu	Thr	Ala	Leu	Gly	Pro	Pro	Gln	Pro	Thr	Asn	Leu
632	•				405				•	410					415	
	Asp	Ser	Thr	Ala	Phe	Trp	Glu	Glv	Phe	Ser	His	Pro	Glu	Thr	Arq	Pro
636	•			420		•		•	425					430	-	
	Lvs	Leu	Asp	Glu	Glv	Ser	Val	Leu	Leu	Leu	His	Arq	Thr	Leu	Gly	Asp
640	•		435		•			440				_	445		•	-
	Lvs	Asp	Ala	Ser	Ara	Val	Gln	Asn	Leu	Val	Ser	Ser	Leu	Pro	Leu	Pro
644	-	450					455					460	•			
647	Glu	Tyr	Cys	Ala	His	Gln	Gly	Lys	Leu	Asn	Leu	Ala	Ser	Tyr	Leu	Pro
	465		•			470	•	•			475			•		480
		Glv	Leu	Thr	Leu	His	Pro	Leu	Glu	Pro	Gln	Leu	Trp	Ala	Ala	Tyr
652					485					490	•		•		495	•
-	Glv	Val	Asn	Ser	His	Arq	Glv	His	Leu	Glv	Thr	Lvs	Asn	Leu	Cys	Val
656	,			500		5	3		505	2		-3-		510	- 4	
	Glu	Val	Ser		Leu	Ile	Ser	Ile	Leu	Va1	His	Ala	Glu	Ala	Gln	Leu
660			515	<u>-</u>				520					525			
	Pro	Pro		Tvr	Ara	Ala	Gln		asa	Phe	Leu	Ser		Leu	Asp	Gly
664		530		- , -	9		535	_,_				540	1			1
	Glu		Len	Trn	Ser	Pro		Ser	Gln	Thr	Ser		Val	Tro	His	Val
	545	1				550	,		V		555					560
		Ara	Ala	G] n	Asp		Gln	Ara	Ile	Ara		Phe	Lev	Gln	Met	
672		~~ Y		0111	565		0111	3		570	3			~	575	
	Cvo	Pro	Δla	Glv		Glv	Thr	Leu	Glu		Glv	Ala	Pro	Glv		Cvs
676	Cys		ALU	580	CI	O+ y	****	⊿ ¢u	585		O _T y	n ₄ u	-10	590		-10
070				200					دور					2,70		

DATE: 05/02/2006

```
PATENT APPLICATION: US/10/712,629C
                                                             TIME: 14:30:25
                    Input Set : A:\PTO.TS.txt
                    Output Set: N:\CRF4\05022006\J712629C.raw
     679 Tyr Leu Asp Ala Gly Leu Arg Arg Arg Leu Arg Glu Glu Trp Gly Val
                595
     683 Ser Cys Trp Thr Leu Leu Gln Ala Pro Gly Glu Ala Val Leu Val Pro
                                 615
     687 Ala Gly Ala Pro His Gln Val Gln Gly Leu Val Ser Thr Ile Ser Val
                            630
                                                635
     688 625
     691 Thr Gln His Phe Leu Ser Pro Glu Thr Ser Ala Leu Ser Ala Gln Leu
                                            650
                        645
     695 Cys His Gln Gly Ala Ser Leu Pro Pro Asp His Arg Met Leu Tyr Ala
                                        665
                    660
     699 Gln Met Asp Arg Ala Val Phe Gln Ala Val Lys Ala Ala Val Gly Ala
                675
    703 Leu Gln Glu Ala Lys
    707 <210> SEQ ID NO: 18
708 <211> LENGTH: (693) 2079(P. 4)
B--> 704
    709 <212> TYPE: PRT) 7 Thi
                                 is a DNA sequen
     710 <213 > ORGANISM: C-terminal portion of hairless protein of mouse (HRt) having amino
acid
W--> 711 residues 490 to 1182
                                                                                 invalid
22137
response
     713 <400> SEQUENCE: 18
     715 gttacccagt gccaaagctg tgtccaggca gctggagagg taggggtact gaccggccac
                                                                              120
     717 teccagaaat caegtaggte acceetggaa gagaageagt tggaggagga ggatteetet
                                                                              180
     719 gccacttccg aagaaggagg aggagggcct ggcccagaag cttcactcaa caagggcctg
                                                                              240
     721 gccaagcacc tgctgagtgg tttgggggac cgactctgcc gcctgctgcg gaaggagcgg
     723 gaggeeettg eetgggeaca gegagaagge caggggeeag eeatgaeaga ggaeageeea
                                                                              300
     725 ggcattccac attgctgcag ccgatgccac cacggactct tcaacaccca ctggagatgt
                                                                              360
                                                                              420
     727 teccaetgta gecaecgget gtgtgtagee tgtggtegea tageeggege tggaaagaae
     729 agggagaaaa caggttetea ggaacageac acagatgaet gegeecagga ggetgggeat
                                                                              480
                                                                              540
     731 getgeetgtt eeetgateet gaeeeagttt gteteeagee aggegetgge agaactgage
                                                                              600
     733 actgtgatgc accaagectg ggccaagttt gacatteggg ggcaetgttt etgecaggtt
                                                                              660
     735 gatqcccqtq tgtgggcccc cggggatggg ggtcagcaga aggaaccaac agagaaaact
                                                                              720
     737 cccccaactc cacaaccttc ctgcaatgga gattccaatc ggaccaagga catcaaagaa
                                                                              780
     739 gagaccccag actocactga gagcccagca gaggacggtg ctggccggtc accoettect
                                                                              840
     741 tgtccctctc tctgtgaget gctagcctct actgctgtca aactctgcct ggggcatgac
     743 cggattcaca tggcctttgc tccggtcacc ccagctctgc ccagtgatga ccgcattacc
                                                                              900
     745 aacatectgg acageattat tgegeaggta gtagaacgga agatecaaga gaaageeetg
                                                                              960
                                                                             1020
     747 gggccaggcc tgcgagcagg gtcaggctta cgcaagggcc tgagccttcc attgtcacca
                                                                             1080
     749 gtgcgaaccc ggctgtctcc tcctggagct ttgctgtggc tgcaggagcc taggcctaag
                                                                             1140
     751 catggettee atetetteea ggaacactgg eggeagggee agecegtgtt agtgteagge
     753 atccagaaga cattgagact tagcctgtgg ggaatggaag cccttgggac acttggtggc
                                                                             1200
                                                                             1260
     757 ttctgggagg gattetetea teetgagaca egteeaaagt tagatgaggg etetgteete
                                                                             1380
     759 ctgctacacc gaaccetggg ggataaggac getagcaggg tgcagaacet tgtctccagc
     761 cttccactcc cagaatactg tgcccaccaa gggaaactca acctagcgtc ctacctcccc
                                                                             1440
                                                                             1500
     763 ctgggcctca cactgcatcc actggagccc cagctctggg cggcctatgg tgtgaactca
     765 caccgtggac acctggggac caagaateta tgcgtggagg tgtctgacct aatcagtate
                                                                             1560
     767 ctggtgcacg ccgaggccca gctgcctccc tggtatcgag cacagaaaga tttcctctca
                                                                             1620
     769 ggcctggatg gggaaggact ctggtctcca gggagccaga ccagcactgt gtggcatgtg
                                                                             1680
     771 ttccgggccc aggatgccca gcgcatccgt cgctttctcc agatggtgtg cccagctgga
                                                                             1740
```

RAW SEQUENCE LISTING

RAW SEQUENCE LISTING DATE: 05/02/2006
PATENT APPLICATION: US/10/712,629C TIME: 14:30:25

Input Set : A:\PTO.TS.txt

Output Set: N:\CRF4\05022006\J712629C.raw

			ccgtatgctt ggcgttacag	-	tggaecggge	rgrgrrccaa	2040 2079 <u></u>
	_	_	tgagacctct	-			1980
777	gtgctggtcc	cggctggggc	gccccatcag	gtgcagggcc	tggtgagcac	aatcagtgtc	1920
775	cggctaagag	aagagtgggg	tgtgagctgc	tggaccctgc	tgcaggctcc	tggggaagcg	1860
773	gcaggaacct	tggagcctgg	tgccccaggc	agctgctact	tggatgcagg	gttgcgccga	1800

see P.5 for more enou

<210> 19 <211> 30 <212> DNA <213> Oligonucleotide primer Mindf (2137 response)	
<400> 19 ccggaattcg tcacccagtg ccaaagctgt	30
<210> 20 <211> 49 <212> DNA	

VERIFICATION SUMMARYDATE: 05/02/2006PATENT APPLICATION: US/10/712,629CTIME: 14:30:26

Input Set : A:\PTO.TS.txt

Output Set: N:\CRF4\05022006\J712629C.raw

L:527 M:259 W: Allowed number of lines exceeded, <213> ORGANISM:

L:704 M:301 E: (44) No Sequence Data was Shown, SEQ ID:17

L:704 M:252 E: No. of Seq. differs, <211> LENGTH:Input:2079 Found:0 SEQ:17

L:711 M:259 W: Allowed number of lines exceeded, <213> ORGANISM:

L:783 M:301 E: (44) No Sequence Data was Shown, SEQ ID:18

L:783 M:252 E: No. of Seq. differs, <211> LENGTH:Input:693 Found:0 SEQ:18